

THE CHANGING MOLECULAR EPIDEMIOLOGY OF HIV-1 IN THAILAND: EMERGENCE OF CRF01_AE/B RECOMBINANT STRAINS

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Background: With HIV-1 vaccine efficacy trials underway and planned, we sought to assess the changing molecular picture of HIV-1 in Thailand through full genome sequencing and analysis of CRF01_AE/B recombinant strains retrieved in recent years from HIV-1 infected populations with different exposures.

Methods: Using genetic subtype screening methods, V3 loop serotyping, or HIV-1 neutralization assay, 16 HIV-1 infected samples with subtype discordant results were drawn from two different cohorts during 1990-2002: a cohort in Thailand with both IDU and heterosexual risk and a US military cohort with heterosexual risk. A near full-length genome was recovered from primary or cocultured PBMC by PCR amplification, sequencing, and phylogenetically analyzed.

Results: We identified 16 recombinant strains from the beginning of the epidemic to date. Among them, 4 shared similar genome structure and were classified as a circulating recombinant form CRF15_01B. Among the remaining 12, the structure varied from very simple, with two recombination breakpoints, to a rather complex structure with 8 breakpoints across the genome. The breakpoints were seen all over the genome, and some of the break-points were found to be common among these recombinants indicating either preferred sites (hotspots) or common parents. Of note, CRF15 strains identified here have similar structure with a recombinant identified by other investigators in IDU from Myanmar, indicating a link between Thai IDU networks and neighboring countries.

Conclusions: Emergence of CRF01_AE/B recombinants, the complexity of their genomes, and the increasing frequency of them in the most recent portion of the epidemic are highly indicative of intermixing between two strains, and ongoing recombination between them and the existing recombinants. The dynamics of Thai epidemic and its links with neighboring countries demand that molecular epidemiology studies continue to track HIV evolution in Thailand.

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CHANGES IN HIV PREVALENCE AMONG YOUNG THAI MEN AS DEFINED BY HEPATITIS C CO-INFECTION AS A MARKER FOR MODE OF TRANSMISSION

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To obtain a better understanding of the evolving HIV-1 epidemic in Thailand, we utilized antibody to hepatitis C virus (HCV) to indicate the mode of HIV-1 transmission. Although the proportion of men with HCV co-infection increased between 1995 and 2000, the prevalence